

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/537,512  
Source: P4/10  
Date Processed by STIC: 6/14/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 06/14/2005

PATENT APPLICATION: US/10/537,512

TIME: 09:05:02

Input Set : A:\53529-5007-02-US Sequence Listing.txt

Output Set: N:\CRF4\06142005\J537512.raw

3 <110> APPLICANT: LYNCH, Berkley  
 4 NOCKA, Karl  
 5 FUKS, Bruno  
 7 <120> TITLE OF INVENTION: Methods for the identification of agents for the treatment  
 of  
 8 seizures, neurological diseases, endocrinopathies and hormonal  
 9 diseases  
 11 <130> FILE REFERENCE: 53529-5007-02-US  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/537,512  
 C--> 13 <141> CURRENT FILING DATE: 2005-06-03  
 13 <150> PRIOR APPLICATION NUMBER: PCT/US2003/038122  
 14 <151> PRIOR FILING DATE: 2003-12-02  
 16 <150> PRIOR APPLICATION NUMBER: US 60/430,372  
 17 <151> PRIOR FILING DATE: 2002-12-03  
 19 <150> PRIOR APPLICATION NUMBER: US 60/506,764  
 20 <151> PRIOR FILING DATE: 2003-09-30  
 22 <160> NUMBER OF SEQ ID NOS: 16  
 24 <170> SOFTWARE: PatentIn version 3.3  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 2229  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Homo sapiens  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (1)..(2229)  
 36 <400> SEQUENCE: 1  
 37 atg gaa gag ggc ttc cga gac cgg gca gct ttc atc cgt ggg gcc aaa 48  
 38 Met Glu Glu Gly Phe Arg Asp Arg Ala Ala Phe Ile Arg Gly Ala Lys  
 39 1 5 10 15  
 41 gac att gct aag gaa gtc aaa aag cat gcg gcc aag aag gtg gtg aag 96  
 42 Asp Ile Ala Lys Glu Val Lys Lys His Ala Ala Lys Lys Val Val Lys  
 43 20 25 30  
 45 ggc ctg gac aga gtc cag gac gaa tat tcc cga aga tcg tac tcc cgc 144  
 46 Gly Leu Asp Arg Val Gln Asp Glu Tyr Ser Arg Arg Ser Tyr Ser Arg  
 47 35 40 45  
 49 ttt gag gag gag gat gat gat gat gac ttc cct gct ccc agt gat ggt 192  
 50 Phe Glu Glu Glu Asp Asp Asp Asp Phe Pro Ala Pro Ser Asp Gly  
 51 50 55 60  
 53 tat tac cga gga gaa ggg acc cag gat gag gag gaa ggt ggt gca tcc 240  
 54 Tyr Tyr Arg Gly Glu Gly Thr Gln Asp Glu Glu Glu Gly Gly Ala Ser  
 55 65 70 75 80  
 57 agt gat gct act gag ggc cat gac gag gat gat gag atc tat gaa ggg 288  
 58 Ser Asp Ala Thr Glu Gly His Asp Glu Asp Asp Glu Ile Tyr Glu Gly  
 59 85 90 95

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61	gaa tat cag ggc att ccc cgg gca gag tct ggg ggc aaa ggc gag cgg	336
62	Glu Tyr Gln Gly Ile Pro Arg Ala Glu Ser Gly Gly Lys Gly Glu Arg	
63	100 105 110	
65	atg gca gat ggg gcg ccc ctg gct gga gta agg ggg ggc ttg agt gat	384
66	Met Ala Asp Gly Ala Pro Leu Ala Gly Val Arg Gly Gly Leu Ser Asp	
67	115 120 125	
69	ggg gag ggt ccc cct ggg ggc cgg ggg gag gca caa cga cgg aaa gaa	432
70	Gly Glu Gly Pro Pro Gly Gly Arg Gly Glu Ala Gln Arg Arg Lys Glu	
71	130 135 140	
73	cga gaa gaa ctg gcc caa cag tat gaa gcc atc cta cgg gag tgt ggc	480
74	Arg Glu Glu Leu Ala Gln Tyr Glu Ala Ile Leu Arg Glu Cys Gly	
75	145 150 155 160	
77	cac ggc cgc ttc cag tgg aca ctg tat ttt gtg ctt ggt ctg gcg ctg	528
78	His Gly Arg Phe Gln Trp Thr Leu Tyr Phe Val Leu Gly Leu Ala Leu	
79	165 170 175	
81	atg gct gac ggt gtg gag gtc ttt gtg gtg ggc ttc gtg ctg ccc agc	576
82	Met Ala Asp Gly Val Glu Val Phe Val Val Gly Phe Val Leu Pro Ser	
83	180 185 190	
85	gct gag aaa gac atg tgc ctg tcc gac tcc aac aaa ggc atg cta ggc	624
86	Ala Glu Lys Asp Met Cys Leu Ser Asp Ser Asn Lys Gly Met Leu Gly	
87	195 200 205	
89	ctc atc gtc tac ctg ggc atg atg gtg gga gcc ttc ctc tgg gga ggt	672
90	Leu Ile Val Tyr Leu Gly Met Met Val Gly Ala Phe Leu Trp Gly Gly	
91	210 215 220	
93	ctg gct gac cgg ctg ggt cgg agg cag tgt ctg ctc atc tcg ctc tca	720
94	Leu Ala Asp Arg Leu Gly Arg Arg Gln Cys Leu Leu Ile Ser Leu Ser	
95	225 230 235 240	
97	gtc aac agc gtc ttc gcc ttc ttc tca tct ttt gtc cag ggt tac ggc	768
98	Val Asn Ser Val Phe Ala Phe Phe Ser Ser Phe Val Gln Gly Tyr Gly	
99	245 250 255	
101	act ttc ctc ttc tgc cgc cta ctt tct ggg gtt ggg att gga ggg tcc	816
102	Thr Phe Leu Phe Cys Arg Leu Leu Ser Gly Val Gly Ile Gly Gly Ser	
103	260 265 270	
105	atc ccc att gtc ttc tcc tat ttc tcc gag ttt ctg gcc cag gag aaa	864
106	Ile Pro Ile Val Phe Ser Tyr Phe Ser Glu Phe Leu Ala Gln Glu Lys	
107	275 280 285	
109	cga ggg gag cat ttg agc tgg ctc tgc atg ttt tgg atg att ggt ggc	912
110	Arg Gly Glu His Leu Ser Trp Leu Cys Met Phe Trp Met Ile Gly Gly	
111	290 295 300	
113	gtg tac gca gct gct atg gcc tgg gcc atc atc ccc cac tat ggg tgg	960
114	Val Tyr Ala Ala Ala Met Ala Trp Ala Ile Ile Pro His Tyr Gly Trp	
115	305 310 315 320	
117	agt ttt cag atg ggt tct gcc tac cag ttc cac agc tgg agg gtc ttc	1008
118	Ser Phe Gln Met Gly Ser Ala Tyr Gln Phe His Ser Trp Arg Val Phe	
119	325 330 335	
121	gtc ctc gtc tgc gcc ttt cct tct gtg ttt gcc att ggg gct ctg acc	1056
122	Val Leu Val Cys Ala Phe Pro Ser Val Phe Ala Ile Gly Ala Leu Thr	
123	340 345 350	
125	acg cag cct gag agc ccc cgt ttc ttc cta gag aat gga aag cat gat	1104

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126	Thr	Gln	Pro	Glu	Ser	Pro	Arg	Phe	Phe	Leu	Glu	Asn	Gly	Lys	His	Asp	
127			355					360					365				
129	gag	gcc	tgg	atg	gtg	ctg	aag	cag	gtc	cat	gat	acc	aac	atg	cga	gcc	1152
130	Glu	Ala	Trp	Met	Val	Leu	Lys	Gln	Val	His	Asp	Thr	Asn	Met	Arg	Ala	
131		370					375					380					
133	aaa	gga	cat	cct	gag	cga	gtg	ttc	tca	gta	acc	cac	att	aag	acg	att	1200
134	Lys	Gly	His	Pro	Glu	Arg	Val	Phe	Ser	Val	Thr	His	Ile	Lys	Thr	Ile	
135	385					390					395					400	
137	cat	cag	gag	gat	gaa	ttg	att	gag	atc	cag	tgc	gac	aca	ggg	acc	tgg	1248
138	His	Gln	Glu	Asp	Glu	Leu	Ile	Glu	Ile	Gln	Ser	Asp	Thr	Gly	Thr	Trp	
139				405						410					415		
141	tac	cag	cgc	tgg	ggg	gtc	cgg	gcc	ttg	agc	cta	ggg	ggg	cag	gtt	tgg	1296
142	Tyr	Gln	Arg	Trp	Gly	Val	Arg	Ala	Leu	Ser	Leu	Gly	Gly	Gln	Val	Trp	
143			420					425						430			
145	ggg	aat	ttt	ctc	tcc	tgt	ttt	ggt	ccc	gaa	tat	cgg	cgc	atc	act	ctg	1344
146	Gly	Asn	Phe	Leu	Ser	Cys	Phe	Gly	Pro	Glu	Tyr	Arg	Arg	Ile	Thr	Leu	
147			435					440					445				
149	atg	atg	atg	ggt	gtg	tgg	ttc	acc	atg	tca	ttc	agc	tac	tat	ggc	ctg	1392
150	Met	Met	Met	Gly	Val	Trp	Phe	Thr	Met	Ser	Phe	Ser	Tyr	Tyr	Gly	Leu	
151			450				455					460					
153	acc	gtc	tgg	ttt	cct	gac	atg	atc	cgc	cat	ctc	cag	gca	gtg	gac	tac	1440
154	Thr	Val	Trp	Phe	Pro	Asp	Met	Ile	Arg	His	Leu	Gln	Ala	Val	Asp	Tyr	
155	465					470					475					480	
157	gca	tcc	cgc	acc	aaa	gtg	ttc	ccc	ggg	gag	cgc	gta	gag	cat	gta	act	1488
158	Ala	Ser	Arg	Thr	Lys	Val	Phe	Pro	Gly	Glu	Arg	Val	Glu	His	Val	Thr	
159				485						490					495		
161	ttt	aac	ttc	acg	ttg	gag	aat	cag	atc	cac	cga	ggc	ggg	cag	tac	ttc	1536
162	Phe	Asn	Phe	Thr	Leu	Glu	Asn	Gln	Ile	His	Arg	Gly	Gly	Gln	Tyr	Phe	
163			500					505						510			
165	aat	gac	aag	ttc	att	ggg	ctg	cgg	ctc	aag	tca	gtg	tcc	ttt	gag	gat	1584
166	Asn	Asp	Lys	Phe	Ile	Gly	Leu	Arg	Leu	Lys	Ser	Val	Ser	Phe	Glu	Asp	
167			515				520					525					
169	tcc	ctg	ttt	gaa	gag	tgt	tat	ttt	gag	gat	gtc	aca	tcc	agc	aac	acg	1632
170	Ser	Leu	Phe	Glu	Glu	Cys	Tyr	Phe	Glu	Asp	Val	Thr	Ser	Ser	Asn	Thr	
171			530				535					540					
173	ttt	ttc	cgc	aac	tgc	aca	ttc	atc	aac	act	gtg	ttc	tat	aac	act	gac	1680
174	Phe	Phe	Arg	Asn	Cys	Thr	Phe	Ile	Asn	Thr	Val	Phe	Tyr	Asn	Thr	Asp	
175	545					550					555					560	
177	ctg	ttc	gag	tac	aag	ttt	gtg	aac	agc	cgt	ctg	ata	aac	agt	aca	ttc	1728
178	Leu	Phe	Glu	Tyr	Lys	Phe	Val	Asn	Ser	Arg	Leu	Ile	Asn	Ser	Thr	Phe	
179				565						570					575		
181	ctg	cac	aac	aag	gag	ggc	tgc	ccg	cta	gac	gtg	aca	ggg	acg	ggc	gaa	1776
182	Leu	His	Asn	Lys	Glu	Gly	Cys	Pro	Leu	Asp	Val	Thr	Gly	Thr	Gly	Glu	
183			580						585					590			
185	ggt	gcc	tac	atg	gta	tac	ttt	gtg	agc	ttc	ctg	ggg	aca	ctg	gca	gtg	1824
186	Gly	Ala	Tyr	Met	Val	Tyr	Phe	Val	Ser	Phe	Leu	Gly	Thr	Leu	Ala	Val	
187			595				600					605					
189	ctt	cct	ggg	aat	atc	gtg	tct	gcc	ctg	ctc	atg	gac	aag	atc	ggc	agg	1872
190	Leu	Pro	Gly	Asn	Ile	Val	Ser	Ala	Leu	Leu	Met	Asp	Lys	Ile	Gly	Arg	

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191      610      615      620
193 ctc aga atg ctt gct ggc tcc agc gtg atg tcc tgt gtc tcc tgc ttc      1920
194 Leu Arg Met Leu Ala Gly Ser Ser Val Met Ser Cys Val Ser Cys Phe
195 625      630      635      640
197 ttc ctg tct ttt ggg aac agt gag tcg gcc atg atc gct ctg ctc tgc      1968
198 Phe Leu Ser Phe Gly Asn Ser Glu Ser Ala Met Ile Ala Leu Leu Cys
199      645      650      655
201 ctt ttt ggc ggg gtc agc att gca tcc tgg aat gcg ctg gac gtg ttg      2016
202 Leu Phe Gly Gly Val Ser Ile Ala Ser Trp Asn Ala Leu Asp Val Leu
203      660      665      670
205 act gtt gaa ctc tac ccc tca gac aag agg acc aca gct ttt ggc ttc      2064
206 Thr Val Glu Leu Tyr Pro Ser Asp Lys Arg Thr Thr Ala Phe Gly Phe
207      675      680      685
209 ctg aat gcc ctg tgt aag ctg gca gct gtg ctg ggg atc agc atc ttc      2112
210 Leu Asn Ala Leu Cys Lys Leu Ala Ala Val Leu Gly Ile Ser Ile Phe
211      690      695      700
213 aca tcc ttc gtg gga atc acc aag gct gca ccc atc ctc ttt gcc tca      2160
214 Thr Ser Phe Val Gly Ile Thr Lys Ala Ala Pro Ile Leu Phe Ala Ser
215 705      710      715      720
217 gct gcc ctt gcc ctt ggc agc tct ctg gcc ctg aag ctg cct gag acc      2208
218 Ala Ala Leu Ala Leu Gly Ser Ser Leu Ala Leu Lys Leu Pro Glu Thr
219      725      730      735
221 cgg ggg cag gtg ctg cag tga      2229
222 Arg Gly Gln Val Leu Gln
223      740
226 <210> SEQ ID NO: 2
227 <211> LENGTH: 742
228 <212> TYPE: PRT
229 <213> ORGANISM: Homo sapiens
231 <400> SEQUENCE: 2
233 Met Glu Glu Gly Phe Arg Asp Arg Ala Ala Phe Ile Arg Gly Ala Lys
234 1      5      10      15
237 Asp Ile Ala Lys Glu Val Lys Lys His Ala Ala Lys Lys Val Val Lys
238      20      25      30
241 Gly Leu Asp Arg Val Gln Asp Glu Tyr Ser Arg Arg Ser Tyr Ser Arg
242      35      40      45
245 Phe Glu Glu Glu Asp Asp Asp Asp Phe Pro Ala Pro Ser Asp Gly
246      50      55      60
249 Tyr Tyr Arg Gly Glu Gly Thr Gln Asp Glu Glu Gly Gly Ala Ser
250 65      70      75      80
253 Ser Asp Ala Thr Glu Gly His Asp Glu Asp Asp Glu Ile Tyr Glu Gly
254      85      90      95
257 Glu Tyr Gln Gly Ile Pro Arg Ala Glu Ser Gly Gly Lys Gly Glu Arg
258      100      105      110
261 Met Ala Asp Gly Ala Pro Leu Ala Gly Val Arg Gly Gly Leu Ser Asp
262      115      120      125
265 Gly Glu Gly Pro Pro Gly Gly Arg Gly Glu Ala Gln Arg Arg Lys Glu
266      130      135      140
269 Arg Glu Glu Leu Ala Gln Gln Tyr Glu Ala Ile Leu Arg Glu Cys Gly

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270 145          150          155          160
273 His Gly Arg Phe Gln Trp Thr Leu Tyr Phe Val Leu Gly Leu Ala Leu
274          165          170          175
277 Met Ala Asp Gly Val Glu Val Phe Val Val Gly Phe Val Leu Pro Ser
278          180          185          190
281 Ala Glu Lys Asp Met Cys Leu Ser Asp Ser Asn Lys Gly Met Leu Gly
282          195          200          205
285 Leu Ile Val Tyr Leu Gly Met Met Val Gly Ala Phe Leu Trp Gly Gly
286          210          215          220
289 Leu Ala Asp Arg Leu Gly Arg Arg Gln Cys Leu Leu Ile Ser Leu Ser
290 225          230          235          240
293 Val Asn Ser Val Phe Ala Phe Phe Ser Ser Phe Val Gln Gly Tyr Gly
294          245          250          255
297 Thr Phe Leu Phe Cys Arg Leu Leu Ser Gly Val Gly Ile Gly Gly Ser
298          260          265          270
301 Ile Pro Ile Val Phe Ser Tyr Phe Ser Glu Phe Leu Ala Gln Glu Lys
302          275          280          285
305 Arg Gly Glu His Leu Ser Trp Leu Cys Met Phe Trp Met Ile Gly Gly
306          290          295          300
309 Val Tyr Ala Ala Ala Met Ala Trp Ala Ile Ile Pro His Tyr Gly Trp
310 305          310          315          320
313 Ser Phe Gln Met Gly Ser Ala Tyr Gln Phe His Ser Trp Arg Val Phe
314          325          330          335
317 Val Leu Val Cys Ala Phe Pro Ser Val Phe Ala Ile Gly Ala Leu Thr
318          340          345          350
321 Thr Gln Pro Glu Ser Pro Arg Phe Phe Leu Glu Asn Gly Lys His Asp
322          355          360          365
325 Glu Ala Trp Met Val Leu Lys Gln Val His Asp Thr Asn Met Arg Ala
326          370          375          380
329 Lys Gly His Pro Glu Arg Val Phe Ser Val Thr His Ile Lys Thr Ile
330 385          390          395          400
333 His Gln Glu Asp Glu Leu Ile Glu Ile Gln Ser Asp Thr Gly Thr Trp
334          405          410          415
337 Tyr Gln Arg Trp Gly Val Arg Ala Leu Ser Leu Gly Gly Gln Val Trp
338          420          425          430
341 Gly Asn Phe Leu Ser Cys Phe Gly Pro Glu Tyr Arg Arg Ile Thr Leu
342          435          440          445
345 Met Met Met Gly Val Trp Phe Thr Met Ser Phe Ser Tyr Tyr Gly Leu
346          450          455          460
349 Thr Val Trp Phe Pro Asp Met Ile Arg His Leu Gln Ala Val Asp Tyr
350 465          470          475          480
353 Ala Ser Arg Thr Lys Val Phe Pro Gly Glu Arg Val Glu His Val Thr
354          485          490          495
357 Phe Asn Phe Thr Leu Glu Asn Gln Ile His Arg Gly Gly Gln Tyr Phe
358          500          505          510
361 Asn Asp Lys Phe Ile Gly Leu Arg Leu Lys Ser Val Ser Phe Glu Asp
362          515          520          525
365 Ser Leu Phe Glu Glu Cys Tyr Phe Glu Asp Val Thr Ser Ser Asn Thr
366          530          535          540

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## VERIFICATION SUMMARY

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Input Set : A:\53529-5007-02-US Sequence Listing.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date